

<!--StartFragment-->RESULT 5

ABB75752

ID ABB75752 standard; protein; 708 AA.

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AC ABB75752;

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DT 15-JUN-2007 (revised)

DT 24-JUN-2002 (first entry)

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DE Human gp354 (putative splice variant).

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KW Human; GP354; immunoglobulin; pancreas; central nervous system;

KW diagnosis; gene therapy; pancreatitis; inflammation; tumour; cancer;

KW autoimmune disease; Alzheimer's disease; Parkinson's disease;

KW senile dementia; migraine; epilepsy; neurasthenia; neuropathy;

KW neural degeneration; antiinflammatory; cytostatic; nootropic;

KW immunosuppressive; antiparkinsonian; neuroprotective; antimigraine;

KW anticonvulsant; splice variant; BOND_PC; LRMR5827;

KW LRMR5827 [Homo sapiens]; GO7155; GO16020; GO16021.

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OS Homo sapiens.

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FH Key Location/Qualifiers

FT Peptide 1. .21

FT /label= Signal_peptide

FT Protein 22. .708

FT /label= Mature_protein

FT Domain 22. .510

FT /note= "extracellular domain"

FT Domain 38. .109

FT /note= "Ig domain"

FT Domain 139. .206

FT /note= "Ig domain"

FT Domain 242. .293

FT /note= "Ig domain"

FT Domain 326. .377

FT /note= "Ig domain"

FT Domain 413. .488

FT /note= "Ig domain"

FT Domain 511. .533

FT /note= "transmembrane domain"

FT Domain 534. .708

FT /note= "intracellular domain"

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PN WO200198360-A2.

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PD 27-DEC-2001.

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PF 22-JUN-2001; 2001WO-US019904.

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PR 22-JUN-2000; 2000US-0213611P.

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PA (BIOJ) BIOGEN INC.

PA (CARU/) CARULLI J P.

PA (LUKA/) LUKASHIN A V.

PA (KILB/) KILBURN D R.

PA (SUNC/) SUN C.

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PI Carulli JP, Lukashin AV, Kilburn DR, Sun C;

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DR WPI; 2002-329171/36.

N-PSDB; ABL53876;
PC:NCBI; gi55735519.
PC:SWISSPROT; Q6UWL6.
XX
PT Novel nucleic acid sequence encoding a member of immunoglobulin
PT superfamily, designated GP354, useful for the treatment of Alzheimer's
PT disease, Parkinson's disease, senile dementia, migraine and epilepsy.
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PS Claim 17; Fig 7; 163pp; English.
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CC The present sequence is that of human GP354 (see ABB75752), a novel
CC member of the immunoglobulin superfamily. The sequence is deduced from
CC gp354 cDNA (see ABL53876), but differs from the gene-derived protein
CC sequence (see ABB75751), e.g. at amino acid positions 195, 196, 539 and
CC 540, suggesting allelic variation or alternative splicing. GP354 is a
CC pancreas-enriched integral membrane protein, also detected at low levels
CC in the central nervous system (CNS). Its protein structure and tissue
CC distribution indicate a role in cell-cell recognition, binding,
CC signalling and adhesion events in the pancreas and CNS. The invention
CC provides GP354 polypeptides and gp354 polynucleotides, as well as
CC vectors, host cells, antibodies and related diagnostic and therapeutic
CC methods. Claimed compositions comprising a gp354 nucleic acid or GP354
CC polypeptide are used in the treatment of pancreatic injury and abnormal
CC or disease conditions that relate to the pancreas, such as acute or
CC chronic pancreatitis, pancreatic inflammation, pancreatic necrosis,
CC exocrine insufficiency, pancreatic endocrine and hormonal imbalance,
CC pancreatic tumours and associated cancers, and autoimmune disorders which
CC affect the pancreas. They are also used in the treatment of an injury to
CC the CNS and abnormal or disease conditions that relate to the CNS,
CC including Alzheimer's disease, Parkinson's disease, senile dementia,
CC migraine, epilepsy, neuritis, neurasthenia, neuropathy, neural
CC degeneration and neural tumours (all claimed)
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 708 AA;

Query Match 85.6%; Score 3156.5; DB 5; Length 708;
Best Local Similarity 84.3%; Pred. No. 2.7e-212;
Matches 594; Conservative 40; Mismatches 66; Indels 5; Gaps 2;

Qy	1	MLASALLVFLCCFKFHAGGSSPHFLQQPEDVMVLLGGEARLPCALGAYRGLVQWTKDGLAL	60
Db	4	MRVPALLVLLFCFRGRAGSPHFLQQPEDLVLLGGEARLPCALGAYWGLVQWTKSGLAL	63
Qy	61	GGERDLPGWSRYWISGNISASGQHDHLHKVPELEDEASYEQCASQAGLRSRPAQLHVMVPP	120
Db	64	GGQDLPGWSRYWISGNAAGQHDHLHTRVPELEDEASYEQCATQAGLRSRPAQLHVLVPP	123
Qy	121	EAPQVLGGPSVSLVAGVPGNLTCRSRGDSRPAPELLWFRDGIRLDASSFHQTTLKDKATG	180
Db	124	EAPQVLGGPSVSLVAGVPGNLTCRSRGDARPTPELLWFRDGLVLDGATFHQTTLKEGTPG	183
Qy	181	TVENTLFLTPSSHDDGATILICRARSQALPTGRDTAVTILSLQYPPMVTLSAEPQTQVEGEK	240
Db	184	SVESTLFLTPSSHDDGATFVCRARSQALPTGRDTAITLSLQYPPVLTLSASPHYTQVEGEK	243
Qy	241	VTFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVADATFLTEPVSCVSNVAGSANRS	300
Db	244	VIFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVADASFLETPVSCVSNVAGSANRS	303

Qy	301	TALEVYIGPILQAKPKSVSDVDGKDAFSCVWRGNPLRITWTWRMGGSQVLSSSGPTLRLP	360
Db	304	TALDVLFGPILQAKPEFVSDVDGDAFSCAWRGNPLRPTWTWRGGAQVLGSGATLRLP	363
Qy	361	SVALEDAGDYVCRAEPRRTGLGGGKAQRLTVNAPPVVTALQPAPAFLRGPRLQCVVFA	420
Db	364	SVGPEDAGDYVCRAEAGLSGLRGAAEARLTVNAPPVVTALHSAPAFLRGPRLQCLVFA	423
Qy	421	SPAPDSVVNSWDEGFLAEGSLGRFLVEAFPAPAEVGGQGGLISVLHISGTQESDFTTGF	480
Db	424	SPAPDAVVNSWDEGFLAEGSQGRFLVETFPAPESRGLGPGILISVLHISGTQESDFSRSF	483
Qy	481	NCSARNRLGEGRVQIHLGRRDLLPTVRIVAGAASAATSLLMVITGVVLCWRH---GSL	536
Db	484	NCSARNRLGEGGAQASLGRDLLPTVRIVAGVAAATTTLLMVITGVALCWRHSAKASAF	543
Qy	537	SKQKNLVRIPGSSSEGSSSRGP-EEETGSSEDRGPVIVTHDSDLVLEEKEALETKDPTNGY	595
Db	544	SEQKNLMRIPGSSDGSSSRGPEEETGSREDRGPVIVTHDSDLVLEEGETLETKDPTNGY	603
Qy	596	YKVRGVSVLSLGEAPGGGLFLPPSPILPGTPTYTYDFKPHLDLVPPCRLRYRARGYLT	655
Db	604	YKVRGVSVLSLGEAPGGGLFLPPSPILPGPTPTFYDFNPHLMVPPCRLRYRARGYLT	663
Qy	656	TPHPRAFTSYMKPTSFPGPDLSSTPPFPYATLSPPSHQLRQTHV 700	
Db	664	TPHPRAFTSYIKPTSFPGPDLAGTPPPFYAAFTPSGPHRLQTHV 708	